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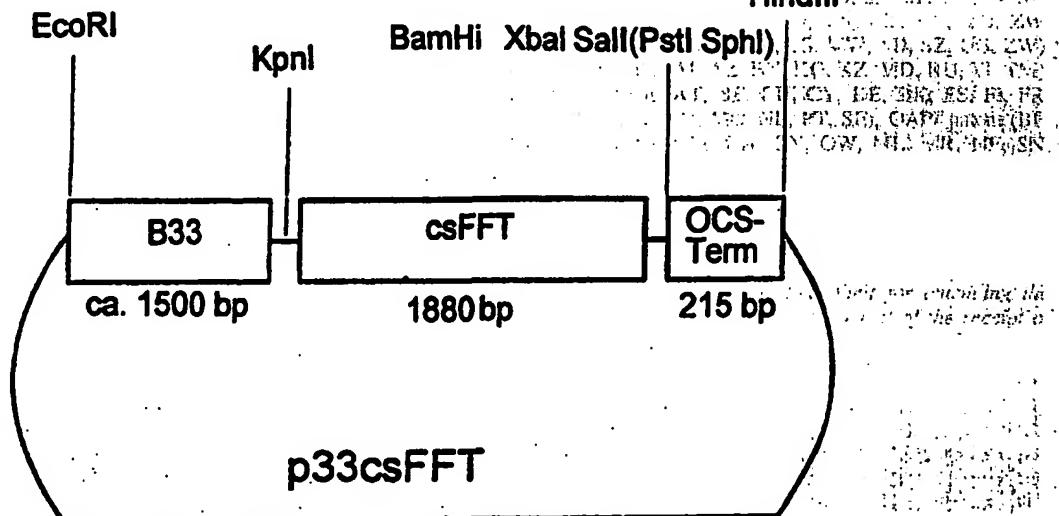
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(54) Title: **NUCLEIC ACID MOLECULES WHICH ENCODE PROTEINS HAVING FRUCTOSYL TRANSFERASE ACTIVITY AND METHODS FOR PRODUCING LONG-CHAIN INULIN**



(57) Abstract

Nucleic acid molecules are described encoding proteins with the enzymatic activity of a fructosyl transferase. These enzymes are fructosyl transferases (FFT). Moreover, vectors and host cells are described containing the nucleic acid molecules of the invention, in particular transformed plant cells, plant tissue and plants regenerable therefrom, which express the described FFT. Furthermore, methods for the production of long-chain inulin by using the described proteins, hosts, in particular the plant cells and/or FFT produced by them, are described.

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## Nucleic acid molecules which encode proteins having fructosyl transferase activity and methods for producing long-chain inulin

The present invention relates to nucleic acid molecules encoding proteins with the enzymatic activity of a fructosyl transferase (FFT). The invention also relates to vectors containing such nucleic acid molecules as well as to host cells transformed with said nucleic acid molecules, in particular plant cells, plant tissue and plants. Moreover, methods for the production of transgenic plants are described which synthesize long-chain inulin due to the introduction of nucleic acid molecules encoding an FFT. The present invention also relates to methods of producing FFT and to the production of long-chain inulin in various host organisms, in particular plants, as well as to in vitro methods for producing long-chain inulin by means of the FFT of the invention. The present invention further relates to the host cells of the invention and to the inulin obtainable by the processes of the present invention.

Water-soluble, linear polymers allow for a variety of applications, for example for increasing the viscosity in aqueous systems, as detergents, as suspending agents or for speeding up sedimentation, for complexing and, however, also for binding water. Polymers which are based on saccharides, such as fructosyl polysaccharides, are particularly interesting raw materials as they are biodegradable.

Apart from their application as regenerable raw materials for the industrial production and processing, fructosyl polymers are also to be considered as additives in foodstuffs, for example as sweeteners. For various uses, polymers with varying chain-lengths are needed. Whereas short- and medium-chain polymers are particularly preferred in the food processing industry, polymers with a high degree of polymerization (DP) are needed for technical uses, such as the production of surfactants.

So far only methods for producing long-chain fructan polysaccharides in plants have been described in which fructosyl transferases of bacterial origin are expressed. Most bacterial fructosyl transferases synthesize levan, a  $\beta$ -2,6 linked fructosyl polymer which has numerous  $\beta$ -2,1-branchings. Due to its numerous branchings levan has decisive disadvantages when it comes to technical processing and is therefore considerably less significant as a technical raw material than inulin. Up to now, only one bacterial gene is known, the gene product of which is involved in the synthesis of inulin, namely the ftf gene from *Streptococcus mutans*. It is in principle possible to express the gene in plants if the gene has previously been genetically engineered. However, the inulin yield obtained from transgenic plants is so low that the economic utilization of the transgenic plants is out of question.

Furthermore, a method for producing transgenic plants expressing fructosyl transferases from *Helianthus tuberosus* is known. The expression of these genes in transgenic plants leads to the production of inulin with an average degree of polymerization of DP=6 to DP=10. Polymers with this degree of polymerization may not be referred to as long-chain inulin. Inulin with an average DP=6 to DP=10 is unsuitable for most technical uses.

Methods for an economic production of long-chain inulin in plants or for synthesizing enzymes for the production of long-chain inulin are not known.

PCT/US89/02729 describes the possibility of synthesizing carbohydrate polymers, in particular dextran or polyfructose, in transgenic plant cells, specifically in the fruits of transgenic plants. In order to produce plants modified in such a way, the use of levan sucrases from microorganisms, in particular from *Aerobacter levanicum*, *Streptococcus salivarius* and *Bacillus subtilis*, or of dextran sucrases from *Leuconostoc mesenteroides* is proposed. Neither the formation of the active enzymes nor that of levan or dextran or the production of transgenic plants is described. PCT/EP93/02110 discloses a method for producing transgenic plants expressing the lsc gene of the levan sucrase from the gram-negative bacterium *Erwinia amylovora*. The plants produce a high-molecular, strongly branched levan. PCT/NL93/00279 describes the transformation of plants with chimeric genes containing the sacB gene from *Bacillus subtilis* or the ftf gene from *Streptococcus*.

*mutans*. Transgenic plants expressing the sacB gene produce a branched levan. Plants expressing the ftf gene synthesize high-molecular inulin; the yield, however, is so low that an economic utilization is out of question. PCT/NL96/00012 discloses DNA sequences encoding enzymes synthesizing carbohydrate polymers as well as the production of transgenic plants by means of these DNA sequences. The disclosed sequences are derived from *Helianthus tuberosus*. According to PCT/NL96/00012, the disclosed sequences may be used in order to modify the fructan profile of petunia and potato, but also of *Helianthus tuberosus* itself. When expressing the SST and the FFT gene in transgenic plants, it is possible to produce inulin. The average degree of polymerization of inulin, however, ranges between DP=6 and DP=10. The production of high-molecular inulin is not possible by means of the method described in PCT/NL96/00012. PCT/EP97/02195 describes a method for producing transgenic, inulin-producing plants by means of the ftf gene from *Streptococcus mutans*. The yield of high-molecular inulin is low, as is the case with the plants described in PCT/NL93/00279. DE 197 08 774.4 describes the production of short-chain inulin by means of enzymes exhibiting fructosyl polymerase activity. The short-chain inulin may be produced in transgenic plants. The yield of short-chain inulin is high and in potato it corresponds to the cellular content of sucrose. The production of long-chain inulin, however, is not described.

The synthesis of inulin in plants has been thoroughly examined (Pollock & Chatterton, Fructans, The Biochemistry of Plants Vol. 14 (1988), Academic Press, pp. 109-140). However, the inulin occurring naturally in plants is short-chain fructan with a maximum degree of polymerization of approximately DP=35 (Pollock & Chatterton, 1988, loc.cit.). Synthesis and metabolism of fructans in plants are based on the activity of at least three enzymes: a sucrose-dependent sucrose-fructosyl transferase (SST) forming the tri-saccharide kestose, a fructan-dependent fructan-fructosyl transferase (FFT) which transfers fructosyl residues from fructan molecules with a minimum degree of polymerization of DP=3 (kestose) to sucrose and higher fructans, and a fructan exohydrolase (FEH) which removes fructose residues from fructan molecules. It is not known whether differences in the average molecular weight of the inulin in various plant species, for example about  $2 \times 10^3$  in the case of

*Allium cepa* and  $5 \times 10^3$  in the case of *Helianthus tuberosus*, are based on the different properties of their SST, FFT or FEH.

For this reason it is not possible in view of the present knowledge relating to the inulin synthesis in plants to identify suitable DNA sequences by means of which high-molecular inulin might be synthesized in plants in economically interesting amounts.

Thus, the technical problem underlying the present invention is to provide nucleic acid molecules and methods which allow for the production of genetically modified organisms, in particular plants, capable of forming long-chain inulin.

This problem is solved by the provision of the embodiments characterized in the claims.

Therefore, the present invention relates to nucleic acid molecules encoding proteins with the enzymatic activity of an FFT, selected from the group consisting of

- (a) nucleic acid molecules encoding a protein comprising the amino acid sequence indicated under SEQ ID No. 2 and SEQ ID No. 4;
- (b) nucleic acid molecules comprising the nucleotide sequence indicated under SEQ ID No. 1 or SEQ ID No. 3 or a corresponding ribonucleotide sequence;
- (c) nucleic acid molecules which hybridize to a complementary strand of the nucleic acid molecules mentioned under (a) or (b) under stringent conditions; and
- (d) nucleic acid molecules comprising a fragment of the nucleotide sequence of (a), (b) or (c).

In the context of the present invention a fructosyl transferase (FFT) is a protein capable of catalyzing the formation of  $\beta$ -2,1-glycosidic and/or  $\beta$ -2,6-glycosidic bonds between fructose units. Thereby, a fructosyl residue to be transferred may be derived from 1-kestose or from a fructan polymer. In connection with the present invention, a high-molecular fructan is a polymer the molecules of which contain an average number of more than 20, preferably more than 25 and even more preferably

at least 32 fructosyl residues. Furthermore, the high-molecular fructan is preferably a polymer the molecules of which contain on the average less than 3000, more preferably less than 300 and particularly preferred less than 100 fructosyl residues. The fructosyl residues may be either glycosidically linked by  $\beta$ -2,1 bonds or by  $\beta$ -2,6 bonds. In the case of inulin the residues are generally linked by  $\beta$ -2,1 glycosidic bonds. To a low degree, also  $\beta$ -2,6-bonds may occur, in particular by less than 5%, preferably by less than 3%, more preferably by less than 1.5% and most preferably by less than 0.5%. The fructosyl polymer may carry at its end a glucose residue which is linked via the C-1 OH-group of the glucose and the C-2 OH-group of a fructosyl residue. In this case, a sucrose molecule is also contained in the fructosyl polymer.

Surprisingly, high amounts of high-molecular inulin are formed during the expression of the nucleic acid molecules of the invention in transformed plants. The inulin formed in the plants exhibits an average degree of polymerization of clearly more than DP=20. This was unexpected since a similar enzyme from *Helianthus tuberosus* is involved in the synthesis of inulin with an average degree of polymerization of less than DP=20 in transgenic plants (PCT/NL96/00012).

The nucleic acid molecules of the invention may be DNA as well as RNA molecules. Corresponding DNA molecules are for example genomic DNA or cDNA molecules. The nucleic acid molecules of the invention may be isolated from natural sources, preferably from artichoke, or they may be synthesized according to known methods. By means of conventional molecular-biological techniques it is possible (see e.g. Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2<sup>nd</sup> edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) to introduce various mutations into the nucleic acid molecules of the invention, which leads to the synthesis of proteins with probably modified biological properties. In this respect, it is possible on the one hand to produce deletion mutants, in which nucleic acid molecules are produced by progressing deletions at the 5' or 3' end of the coding DNA sequence. These nucleic acid molecules lead to the synthesis of correspondingly shortened proteins. By means of such deletions at the 5' end of the

nucleotide sequence it is for example possible to identify amino acid sequences which are responsible for the translocation of the enzyme into the vacuole (transit peptides). This allows for the targeted production of enzymes which, due to the removal of the corresponding sequences, are no longer located within the vacuole but within the cytosol, or within other compartments due to the addition of other signal sequences.

On the other hand, it is also conceivable to introduce point mutations at positions in which a modification of the amino acid sequence for example influences the enzyme activity or the regulation of the enzyme. In this manner e.g. mutants may be produced which exhibit a modified  $K_m$  value or which are no longer subject to the regulation mechanisms occurring in the cell, such as allosteric regulation or covalent modification.

Furthermore, mutants may be produced which exhibit a modified substrate or product specificity. Furthermore, mutants with a modified activity-temperature-profile may be produced.

For recombinant DNA manipulation in prokaryotic cells, the nucleic acid molecules of the invention or parts of these molecules may be inserted into plasmids which allow for a mutagenesis or a sequence modification by recombination of DNA sequences. By means of standard techniques (cf. Sambrook et al., 1989, Molecular Cloning: A laboratory manual, 2<sup>nd</sup> edition, Cold Spring Harbor Laboratory Press, NY, USA) base exchanges may be carried out or natural or synthetic sequences may be added. In order to link the DNA fragments to each other, adapters or linkers may be connected with the fragments. Furthermore, manipulations may be used which provide suitable restriction sites or which remove superfluous DNA or restriction sites. If use can be made of insertions, deletions or substitutions, in vitro mutagenesis, primer repair, restriction or ligation may be used. As analyzing method, use is usually made of sequence analysis, restriction analysis or further biochemical-molecular-biological methods.

In the context of the present invention the term "hybridization" means hybridization under conventional conditions, preferably under stringent conditions, as described for example in Sambrook et al., Molecular Cloning, A Laboratory Manual, 2<sup>nd</sup> edition

(1989), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. An example for stringent hybridization conditions is a hybridization in 50% formamide, 5 x SSC, 5 x Denhardt's solution, 40 mM sodium phosphate pH 6.8; 0.5% (w/v) BSA, 1% (w/v) SDS, 0.1 mg/ml herring sperm DNA at 42°C. An example for conventional non-stringent hybridization conditions is a hybridization under the above-described conditions in which, however, 30% formamide is used instead of 50%. Washing conditions in the case of stringent conditions are preferably 0.5 x SSC/0.5% SDS at 60°C and in the case of non-stringent conditions preferably 2 x SSC/0.5% SDS at 56°C.

Nucleic acid molecules which hybridize to the molecules of the invention can e.g. be isolated from genomic or from cDNA libraries produced from corresponding organisms, such as artichoke.

Such nucleic acid molecules may be identified and isolated by using the molecules of the invention or parts of these molecules or, as the case may be, the reverse complements of these molecules, e.g. by hybridization according to standard techniques (see e.g. Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2<sup>nd</sup> edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

As a hybridization probe e.g. nucleic acid molecules may be used which exhibit exactly or basically the nucleotide sequence indicated under SEQ ID No. 1 or SEQ ID No. 3 or parts thereof. The fragments used as hybridization probe may also be synthetic fragments produced by means of the usual synthesis techniques and the sequence of which is basically similar to that of a nucleic acid molecule of the invention.

The molecules hybridizing to the nucleic acid molecules of the invention also comprise fragments, derivatives and allelic variants of the above-described nucleic acid molecules encoding a protein of the invention. "Fragments" are supposed to be parts of the nucleic acid molecules which are long enough in order to encode a protein of the invention. In this context, the term "derivative" means that the sequences of these molecules differ from the sequences of the above-described nucleic acid molecules at one or more positions. However, they exhibit a high degree of homology to these sequences. Homology means a sequence identity of at least 40%, in particular an identity of at least 60%, preferably of more than 80% and most

preferably of more than 90%. The proteins encoded by these nucleic acid molecules exhibit a sequence identity to the amino acid sequence indicated under SEQ ID No. 2 of at least 80%, preferably 85% and particularly preferred of more than 90%, more preferred of more than 95%, even more preferred of more than 97% and most preferred of more than 99%. The deviations from the above-described nucleic acid molecules may, for example, result from deletion, substitution, insertion and/or recombination.

The nucleic acid molecules which are homologous to the above-described molecules and represent derivatives of these molecules, are usually variations of these molecules representing modifications with the same biological function. These may be naturally occurring variations, for example sequences from other organisms, or mutations, whereby these mutations may have occurred naturally or they may have been introduced by means of targeted mutagenesis. Furthermore, the variations may be synthetically produced sequences. The allelic variants may either be naturally occurring variants or synthetically or recombinantly produced variants.

The proteins encoded by the various variants of the nucleic acid molecules of the invention exhibit certain common characteristics such as the enzyme activity, molecular weight, immunological reactivity or conformation or physical properties such as the mobility in gel electrophoresis, chromatographic characteristics, sedimentation coefficients, solubility, spectroscopic properties, stability, pH-optimum, temperature-optimum etc.

In a preferred embodiment the nucleic acid sequences of the invention are derived from artichoke (*Cynara scolymus*).

The invention further relates to vectors containing the nucleic acid molecules of the invention. These are preferably plasmids, cosmids, viruses, bacteriophages and other vectors common in gene technology.

Within the vector of the invention the nucleic acid molecule of the invention is preferably operably linked to regulatory elements which ensure the transcription and synthesis of a translatable RNA in prokaryotic and/or eukaryotic cells.

The expression vectors of the invention allow for the production of long-chain inulin in various host organisms, in particular in prokaryotic or eukaryotic cells such as bacteria, fungi, algae, animal cells and preferably plant cells and plants. Preferred host organisms are in particular yeasts such as e.g. *S. cerevisiae*, and lactic acid bacteria such as *Streptococcus thermophilus*, *Lactobacillus bulgaricus*, *Streptococcus lactis*, *S. cremoris*, *Lactobacillus acidophilus* and *Leuconostoc cremoris*. The encoded enzymes may probably also be used outside of the host organisms for the production of long-chain inulin. Plant cells are particularly preferred.

A survey concerning various expression systems may be found e.g. in Methods in Enzymology 153 (1987), 385-516, in Bitter et al. (Methods in Enzymology 153 (1987), 516-544), Sawers et al., Applied Microbiology and Biotechnology 46 (1996), 1-9, Billmann-Jacobe, Current Opinion in Biotechnology 7 (1996), 500-504, Hockney, Trends in Biotechnology 12 (1994), 456-463, and Griffiths et al., Methods in Molecular Biology 75 (1997), 427-440. Expression systems for yeast have been described in Hensing et al., Antonie van Leeuwenhoek 67 (1995), 261-279, Bussineau et al., Developments in Biological Standardization 83 (1994), 13-19, Gellissen et al., Antonie van Leeuwenhoek 62 (1992), 79-93, Fleer, Current Opinion in Biotechnology 3 (1992), 486-496, Vedvick, Current Opinion in Biotechnology 2 (1991), 742-745, and in Buckholz, BioTechnology 9 (1991), 1067-1072. Expression vectors have been described to a great extent in the prior art. Apart from a selection marker gene and a replication origin ensuring replication in the selected host, they usually contain a bacterial or viral promoter and in most cases a termination signal for transcription. There is at least one restriction site or one polylinker between the promoter and the termination signal which allows to insert a coding DNA sequence. If it is active in the selected host organism, the DNA sequence naturally controlling the transcription of the corresponding gene may be used as promoter sequence. This sequence may also be exchanged with other promoter sequences. Use may also be made of promoters which lead to a constitutive expression of the gene as well as of inducible promoters allowing for a targeted regulation of the expression of

the downstream gene. Bacterial and viral promoter sequences with these properties have been extensively described in the prior art. Regulatory sequences for the expression in microorganisms (such as *E. coli*, *S. cerevisiae*) have been sufficiently described in the prior art. Promoters which allow for a particularly strong expression of the downstream gene are e.g. the T7 promoter (Studier et al., Methods in Enzymology 185 (1990), 60-89), lacuv5, trp, trp-lacUV5 (DeBoer et al., in Rodriguez and Chamberlin (eds.), Promoters, Structure and Function; Praeger, New York (1982), 462-481; DeBoer et al., Proc. Natl. Acad. Sci. USA (1983), 21-25), λp1, rac (Boros et al., Gene 42 (1986), 97-100). Usually, the amounts of protein are highest from the middle towards the end of the logarithmic phase of the microorganisms' growth cycle. For this reason, inducible promoters are preferably used for the synthesis of proteins. These frequently lead to higher protein yields than constitutive promoters. The use of strongly constitutive promoters often leads, via the permanent transcription and translation of the cloned gene, to the loss of energy for other essential cell functions, which slows down the growth of the cell (Bernard R. Glick, Jack J. Pasternak, Molekulare Biotechnologie (1995), Spektrum Akademischer Verlag GmbH, Heidelberg Berlin Oxford, p. 342). Thus, in order to reach an optimum amount of protein a two-stage process is often used. At first, host cells are cultivated under optimum conditions until a relatively high cell density is achieved. In the second stage, transcription is induced depending on the kind of promoter used. In this context, a tac-promoter inducible by lactose or IPTG (= isopropyl-β-D-thiogalacto-pyranosid) is particularly suitable (deBoer et al., Proc. Natl. Acad. Sci. USA 80 (1983), 21-25). Termination signals for the transcription are also described in the prior art.

The transformation of the host cell with the corresponding protein-encoding DNA may generally be carried out by means of standard techniques, such as described by Sambrook et al. (Molecular Cloning: A Laboratory Course Manual, 2<sup>nd</sup> edition (1989), Cold Spring Harbor Press, New York). The cultivation of the host cell takes place in nutrient media which correspond to the respective requirements of the host cells used, particularly considering the pH value, temperature, salt concentration, airing, antibiotics, vitamins, trace elements etc.

The purification of the enzyme produced by the host cells may be carried out by means of conventional purification techniques such as precipitation, ion exchange chromatography, affinity chromatography, gel filtration, HPLC reverse phase chromatography etc.

By modifying the DNA expressed in the host cells, a polypeptide may be produced in the host cell which can easier be isolated from the culture medium due to certain properties. Thus, there is the possibility of expressing the protein to be expressed as a fusion protein with a further polypeptide sequence, the specific binding properties of which allow for the isolation of the fusion protein via affinity chromatography (e.g. Hopp et al., Bio/Technology 6 (1988), 1204-1210; Sassenfeld, Trends Biotechnol. 8 (1990), 88-93).

For expression in plant cells, regulatory elements of the patatin B33 promoter are preferred. Other preferred promoters are the 35S CaMV promoter and the promoter of the alcohol dehydrogenase gene from *Saccharomyces cerevisiae*.

The vectors of the invention may possess further functional units which stabilize the vector within a host organism, e.g. a bacterial replication origin or the 2-micron-DNA for stabilization in *Saccharomyces cerevisiae*. Furthermore, they may contain left and right border sequences of agrobacterial T-DNA, thus enabling a stable integration into the genome of plants.

The vectors of the invention may further contain functional terminators, such as the terminator of the octopin synthase gene from Agrobacteria.

In another embodiment the nucleic acid molecule of the invention is linked to a nucleic acid molecule within the vector of the invention, said nucleic acid molecule encoding a functional signal sequence in order to direct the enzyme to various cell compartments. This modification may for example consist in an addition of an N-terminal signal sequence for the secretion into the apoplast of higher plants; however, any other modification leading to the fusion of a signal sequence to the encoded FFT is also a subject matter of the invention. The nucleic acid molecule contained in the vector of the invention may in particular contain a sequence encoding an amino acid sequence causing secretion. In this context, use is preferably made of the signal peptide of the  $\alpha$ -CGTase from *Klebsiella oxytoca*.

M5A1 (Fiedler et al., J. Mol. Biol. 256 (1996), 279-291) or of a signal peptide as it is encoded by the nucleotides 11529-11618 of the sequence with the gene bank accession number X 86014.

In a particularly preferred embodiment the invention relates to plasmids p35-csFFT and p33-csFFT, the construction of which is described in the examples (Fig. 2 and 4).

In a further embodiment the invention relates to host cells, which transiently or stably contain the nucleic acid molecules or vectors of the invention or are derived from such cells. In this context, a host cell is an organism capable of taking up recombined DNA in vitro and, if applicable, of synthesizing the proteins encoded by the nucleic acid molecules of the invention. The host cells may be prokaryotic as well as eukaryotic cells. They may in particular be microorganisms. In the context of the present invention, these are all bacteria and protists (such as fungi, in particular yeasts and algae) as they are defined e.g. in Schlegel "Allgemeine Mikrobiologie" (Georg Thieme Verlag (1985), 1-2). In connection with prokaryotic host organisms it should be noted that the positive influence of inulin on the growth of certain microorganisms, such as Bifido bacteria, of the human intestinal tract has successfully been shown. Bifido bacteria have been ascribed a healthy effect (see e.g. Gibson et al., Int. Sugar J. 96 (1994), 381-386; Roberfroid et al., J. of Nutrition 128 (1998), 11-19). A tumor-inhibiting effect has also been discussed (see e.g. Reddy et al., Carcinogenesis 18 (1997), 1371-1374; Singh et al., Carcinogenesis 18 (1997), 833-841). For this reason, the host cells of the invention such as yeast (bread) or lactic acid bacteria (yogurt, butter-milk etc.) are suitable for use in the food processing industry.

In a particularly preferred embodiment a host cell of the invention additionally contains a gene encoding a sucrose-dependent sucrose fructosyl transferase (SST). Such sequences were, for example, isolated from artichoke (German patent application DE-A1 197 08 774), Cichorium intibus (de Halleux et al., Plant Physiol.

113 (1997), 1003-1013), *Helianthus tuberosus* (WO 96/21023) and *Allium cepa* (Vijn et al., *Plant Physiol.* 117 (1998), 1507-1513).

The invention in particular relates to transgenic plant cells transformed with a nucleic acid molecule of the invention or containing the vector systems of the invention or derivatives or parts thereof. These are capable of synthesizing enzymes for the production of long-chain inulin due to the introduction of the vector systems of the invention, derivatives or parts of the vector system. The cells of the invention are preferably characterized in that the introduced nucleic acid molecule of the invention is either heterologous with respect to the transformed cell, i.e. it does not naturally occur in these cells or is localized at a different position within the genome than the respective naturally occurring sequence. Moreover, such a transgenic plant cell of the invention preferably contains a DNA sequence encoding a SST.

The present invention further relates to proteins encoded by the nucleic acid molecules of the invention, as well as to methods for their production wherein the host cell of the invention is cultivated under conditions which allow for the synthesis of the protein. The protein is subsequently isolated from the cultivated cells and/or from the culture medium. The invention further relates to an FFT obtainable from the host cell of the invention or by a method of the invention.

The invention further relates to nucleic acid molecules which specifically hybridize to a nucleic acid molecule of the invention, to a molecule complementary thereto or to a part of such molecules. These are preferably oligonucleotides with a length of at least 10, in particular of at least 15 and particularly preferred of at least 50 nucleotides. The oligonucleotides of the invention may for example be used as primers for a PCR reaction. They may also be components of antisense constructs or of DNA molecules encoding suitable ribozymes.

The present invention also relates to a method for the production of transgenic plant cells, plant tissue and plants comprising the introduction of a nucleic acid molecule or vector of the invention into plant cells, plant tissue and plants.

By providing the nucleic acid molecules of the invention it is possible by means of recombinant DNA techniques to produce long-chain inulin in various organisms, in

particular in plants, as it was so far impossible by means of conventional, e.g. breeding methods. By increasing the activity of the FFT of the invention, for example by overexpressing the nucleic acid molecules of the invention, or by providing mutants that are no longer subject to cell-specific regulation mechanisms and/or exhibit distinct temperature dependencies with respect to their activity, it is possible to increase the yield of plants correspondingly modified by means of recombinant DNA techniques.

Thus, it is possible to express the nucleic acid molecules of the invention in plant cells in order to increase the activity of the corresponding FFT, or to introduce it into cells that do not normally express this enzyme. It is furthermore possible to modify the nucleic acid molecules of the invention according to methods known to the skilled person, in order to obtain the FFTs of the invention that are no longer subject to cell-specific regulation mechanisms or which exhibit modified temperature-dependencies, substrate or product specificities.

For this purpose, the skilled person may utilize various plant transformation systems. Thus, the use of T-DNA for transforming plant cells has been intensely examined and described in EP-A-120 516; Hoekema: The Binary Plant Vector System, Offsetdrukkerij Kanters B.V., Albllasserdam (1985), Chapter V, Fraley, Crit. Rev. Plant. Sci., 4, 1-46 and An, EMBO J. 4 (1985), 277-287. For transferring the DNA into the plant cells, plant explants may suitably be co-cultivated with Agrobacterium tumefaciens or Agrobacterium rhizogenes. From the infected plant material (e.g. pieces of leaves, stem segments, roots, but also protoplasts or suspension-cultivated plant cells) whole plants may then be regenerated in a suitable medium which may contain antibiotics or biozides for the selection of transformed cells. The plants obtained in such a way may then be examined as to whether the introduced DNA is present or not. Other possibilities in order to introduce foreign DNA by using the biolistic method or by transforming protoplasts are known to the skilled person (cf. e.g. Willmitzer, L., 1993 Transgenic plants. In: Biotechnology, A Multi-Volume Comprehensive Treatise (H.J. Rehm, G. Reed, A. Pühler, P. Stadler, editors), Vol. 2, 627-659, VCH Weinheim-New York-Basel-Cambridge).

Alternative Systems for the transformation of monocotyledonous plants are the transformation by means of the biolistic approach, the electrically or chemically induced uptake of DNA into protoplasts, the electroporation of partially permeabilized cells, the macro-injection of DNA into inflorescences, the micro-injection of DNA into microspores and pro-embryos by means of swelling (see e.g. Lusardi, Plant J. 5 (1994), 571-582; Paszkowski, Biotechnology 24 (1992), 387-392). Whereas the transformation of dicotyledonous plants by Ti-plasmid-vector systems by means of *Agrobacterium tumefaciens* is a well-established method, more recent studies indicate that the transformation with vectors based on *Agrobacterium* can also be used in the case of monocotyledonous plants (Chan et al., Plant Mol. Biol. 22 (1993), 491-506; Hiei et al., Plant J. 6 (1994), 271-282; Bytebier et al., Proc. Natl. Acad. Sci. USA 84 (1987), 5345-5349; Raineri et al., Bio/Technology 8 (1990), 33-38; Gould et al., Plant Physiol. 95 (1991), 426-434; Mooney et al., Plant, Cell Tiss. & Org. Cult. 25 (1991), 209-218; Li et al., Plant Mol. Biol. 20 (1992), 1037-1048).

Three of the above-mentioned transformation systems have in the past been established for various types of cereals: electroporation of plant tissue, transformation of protoplasts and the DNA-transfer by particle-bombardment into regenerable tissue and cells (review given in: Jähne et al., Euphytica 85 (1995), 35-44). In the corresponding literature the transformation of wheat is described in various ways (reviewed in Maheshwari et al., Critical Reviews in Plant Science 14 (2) (1995), 149-178).

When expressing the nucleic acid molecules of the invention in plants it is in principle possible that the synthesized protein may be localized within any desired compartment of the plant cell. In order to achieve the localization in a particular compartment the sequence ensuring the localization within the vacuole must be deleted and the remaining coding region has, optionally, to be linked to DNA sequences which ensure the localization within the respective compartment. Such sequences are known in the art (see for example Braun, EMBO J. 11 (1992), 3219-3227; Wolter, Proc. Natl. Acad. Sci. USA 85 (1988), 846-850; Sonnewald, Plant J. 1 (1991), 95-106; Rocha-Sosa, EMBO J. 8 (1989), 23-29).

The present invention also relates to transgenic plant cells, plant tissue and plants which were transformed with one or several of the nucleic acid molecules of the invention, as well as to transgenic plant cells derived from cells transformed in such a way. Such cells contain one or several of the nucleic acid molecules of the invention, whereby this/these is/are preferably linked to regulatory DNA elements that ensure transcription in plant cells, in particular with a promoter. Such cells differ from naturally occurring plant cells in that they contain at least one nucleic acid molecule of the invention which does not naturally occur in these cells or in that such a molecule is integrated at a position within the genome of the cell where it does not naturally occur, i.e. in another genomic environment. Since 1-kestose is the natural substrate of FFT and is itself formed in the reaction of a sucrose-dependent sucrose fructosyl transferase (SST) with the sucrose, it is particularly advantageous and probably necessary to provide an SST apart from the nucleic acid molecule, vector or FFT of the invention. Thus, in a preferred embodiment the present invention relates to transgenic plant cells, plant tissue or plants which additionally contain a gene encoding a sucrose-dependent sucrose fructosyl transferase (SST). These may for example be plants or plant cells which already naturally express an SST such as chicory, *Helianthus tuberosus*, or dahlia or plants into which an SST-encoding DNA sequence was introduced by means of recombinant DNA techniques. Said sequence may have been introduced independently or simultaneously with a nucleic acid molecule or vector of the invention.

The transgenic plant cells and plant tissues can be regenerated to whole plants by means of techniques known to the skilled person. The plants obtainable by regenerating the transgenic plant cells of the invention are also a subject matter of the present invention. A further subject matter of the invention are plants which contain the above-described transgenic plant cells. The transgenic plant cells may in principle be any desired kind of plant species, i.e. monocotyledonous as well as dicotyledonous plants. They are preferably useful plants, in particular sucrose-containing plants such as rice, maize, sugar beet, sugar cane or potato, vegetable plants (e.g. tomato, carrot, leek, chicory etc.), feeding or pasture grass, sweet potato, wheat, barley, rape or soy bean.

The invention also relates to propagation material and harvest products of the plants of the invention such as fruits, seeds, tubers, rootstocks, seedlings, cutting, calli, cell cultures etc.

A further subject matter of the invention is the long-chain inulin obtainable from the host cells of the invention, in particular from transgenic plant cells, plant tissues, plants as well as from the propagation material and from the harvest products.

In another embodiment the invention relates to methods for producing long-chain inulin comprising:

- (a) cultivating a host cell, particularly a plant cell, plant tissue or a plant of the invention, under conditions which allow for the production of FFT; and the conversion of 1-kestose, optionally supplied from the outside, or of an equivalent substrate into long-chain inulin; and
- (b) recovering the thus produced inulin from the cultivated host cells, in particular plant cells, tissues or plants, or from the medium.

In a further embodiment the invention relates to a method for the production of long-chain inulin comprising:

- (a) bringing 1-kestose or an equivalent substrate into contact with an FFT of the invention under conditions which allow for the conversion into long-chain inulin; and
- (b) recovering the thus produced inulin.

The recovering of the inulin from various sources, in particular from plant tissue, has for example been described in Gibson et al., Int. Sugar J. 96 (1994), 381-386; Baxa, Czech J. Food Sci. 16 (1998), 72-76; EP-A-787 745; De Leenheer, Carbohydr. Org. Raw Mater. III, Workshop (1996), Meeting Date 1994, 67-92, Verlag VCH Weinheim, Germany and Russian patent RU 2001621C1.

The present invention further relates to an *in vitro* method for producing long-chain inulin by using the substrate sucrose and an enzyme combination from an SST and an FFT of the invention. In a further embodiment the present invention relates to an *in vitro* method for producing inulin by using a mixture containing fructosyl oligomers

and an FFT of the invention. In this context, a fructosyl oligomer is an oligomer consisting of fructose units with a DP of approximately 2 to 7 which may exhibit a glucose residue at its end. When carrying out the method of the invention, recombinantly produced proteins are preferably used. In the context of the present invention these are proteins which were produced by introducing the respective protein-encoding DNA sequence into a host cell and expressing it there. The protein may subsequently be recovered from the host cell and/or from the culture medium. The host cell is preferably a host cell of the invention as defined above. In a preferred embodiment of the method of the invention enzymes are used which were recombinantly produced and secreted into the culture medium by the host cell, so that it is not necessary to disrupt the cells or to further purify the protein since the secreted protein may be obtained from the supernatant. In order to remove the residues of the culture medium, conventional processing techniques may be used such as dialysis, reverse osmosis, chromatographic methods etc. The same holds true for concentrating the protein secreted in the culture medium. The secretion of proteins by microorganisms is normally mediated by N-terminal signal peptides (signal sequence, leader peptide). Proteins with this signal sequence may penetrate the cell membrane of the microorganism. A secretion of proteins may be achieved by linking the DNA sequence encoding this signal peptide to the corresponding enzyme-encoding region. Use is preferably made of the signal peptide of the  $\alpha$ -CGTase from Klebsiella oxytoca M5A1 (Fiedler et al., J. Mol. Biol. 256 (1996), 279-291) or of a signal peptide as it is encoded by the nucleotides 11529-11618 of the sequence deposited in the gene bank with the accession number X86014. The enzymes used in the method of the invention may alternatively be produced not by using microorganisms but by means of an in vitro transcription and translation system which leads to the expression of the proteins. In a particularly preferred embodiment of the invention the FFT is produced from the protoplasts of the leaf tissue in plants.

The invention further relates to inulin which may be formed from a host cell, in particular a plant cell, plant tissue or a plant of the invention or from the propagation material or the harvest product of the plants and plants cells of the invention or

which is obtainable by one of the above-described methods of the invention. This inulin may preferably be used in order to produce surfactants for increasing the viscosity in aqueous systems, as detergent, as a suspending agent, for speeding up sedimentation, for complexing or for binding water.

These or other embodiments have been disclosed and are evident to the skilled person. They are comprised by the description and the examples of the present invention. Further literature that relates to one of the above-mentioned methods, means or uses and that can be applied in the sense of the present invention, may be taken from the prior art, e.g. from public libraries or by utilizing electronic means. Public data bases serve this purpose, as e.g. "Medline" which may be accessed via Internet, e.g. under the address <http://www.ncbi.nlm.nih.gov/PubMed/medline.html>. Further data bases and addresses are known to the person skilled in the art and may be taken from the Internet, e.g. under the address <http://www.lycos.com>. A survey of sources and information regarding biotechnology patents or patent applications can be found in Berks, TIBTECH 12 (1994), 352-364.

**The figures show:**

Figure 1 shows the HPLC analysis of a complete protoplast extract. The protoplasts were transformed with various vectors: A: transformation was carried out with the vector pA7 that does not contain a coding region fused to the CaMV 35S promoter. B: transformation took place with the vector pA7-csFFT which contains the coding region of the fructan:fructan-fructosyl transferase from artichoke fused to the CaMV 35S promoter. C: transformation was carried out with the vector pA7-htFFT which contains the coding region of the fructan:fructan fructosyl transferase from Helianthus tuberosus as a fusion to the CaMV 35S promoter. Before analysis, the complete protoplast extracts were incubated in a mixture of fructosyl oligomers for 12h each. Analysis was carried out as described in Example 1.

Figure 2 shows the construction of the plasmid p35-csFFT

Figure 3 shows the HPLC analysis of transgenic plants which were transformed with the construct p35-csFFT. The analysis shows that long-chain inulin molecules were formed in transgenic plants which express an SST as well as an FFT from artichoke (35S-SST/FFT 22/19).

Figure 4 shows the construction of the plasmid p33-csFFT

Figure 5 shows the HPLC analysis of transgenic plants which were transformed with the construct p33-csFFT. The analysis shows that long-chain inulin molecules were formed in transgenic plants which express an SST as well as an FFT from artichoke (B33-SST/FFT 47).

The Examples illustrate the invention.

**Example 1: Identification, isolation and characterization of a cDNA encoding a fructosyl transferase from artichoke (*Cynara scolymus*)**

Total RNA was isolated from the receptacles of artichoke (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2<sup>nd</sup> edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, USA). Poly(A)+ mRNA was isolated by means of the mRNA isolation system PolyATtract (Promega Corporation, Madison, WI, USA). Complementary DNA (cDNA) was produced from 5µg of this RNA by means of the ZAP-cDNA synthesis kit of Stratagene (Heidelberg) according to the manufacturer's instructions, and 2x10<sup>6</sup> independent recombinant phage clones were obtained. The amplified cDNA library was screened according to standard methods under low stringency conditions by means of the <sup>32</sup>P-labeled DNA fragment corresponding to the cDNA of the SST from artichoke (Not I-fragment of the plasmid pCy21 as described in DE 197 08 774.4). The sequence of the SST from artichoke has been described in DE 197 08 774.4. Positive clones were screened by means of the SST probe under high stringency. Clones which reacted positively during this screening were abandoned since they were evidently SST cDNA. From the residual clones the cDNA insert was isolated by cleaving the plasmid DNA isolated in standard routines (Sambrook et al., 1989), by means of the restriction enzyme NotI and was cloned into the vector pA7. The sticky ends of the NotI fragment were filled in by means of the T4 polymerase. Subsequently, the fragment was ligated into the SmaI site of pA7. The vector pA7 is a derivative of pUC18 (Yanish-Perron, Gene 33 (1985), 103-119) which contains an insert of the 35S promoter of the Cauliflower-Mosaic virus (nucleotide 7146 to 7464 according to Gardner, Nucleic Acids Res. 9 (1981), 2871-2888) between the EcoRI and the SacI site of the polylinker. Apart from the 35S promoter, pA7 contains the polyadenylation signal of gene 3 of the T-DNA of the Ti plasmid pTi ACH 5 (Gielen, EMBO J. 3 (1984), 835-846), nucleotides 11749 to 11939, which was isolated as a Pvu II-Hind III fragment from the plasmid pAGV 40 (Herrera-Estrella, Nature 303 (1983), 209-213) and cloned between the SphI and the Hind III site of the polylinker after adding Sph I linkers to the Pvu II site.

By means of the pA7 derivatives which contained a cDNA from artichoke, tobacco protoplasts were transformed according to the method of Negritiu (Plant Mol. Biol. 8

(1987), 363-373). The transformed protoplasts were cultivated in K3 medium (Nagy and Maliga, Z. Pflanzenphysiologie 78 (1976), 453-455) at 25°C for two days in the dark. Subsequently, the cell extracts were obtained by repeated freezing and thawing. The extracts were incubated with oligofructans (67.5% 1-kestose, 28.4% nystose, 3.6% fructosyl nystose, 0.5% sucrose) for 12h at 28°C and subsequently analyzed by HPLC. The HPLC analysis was carried out with a CarboPac PA 100 anionic exchange column, which was connected to a Dionex DX-300 gradient chromatography system (Dionex, Sunnyvale, CA, USA). Sugar monomers, oligomers and polymers were detected by means of pulsamperometric detection. The detector adjustment for this purpose was:  $T_1 = 0.48s$ ;  $T_2 = 0.12s$ ;  $T_3 = 0.12s$ ;  $E_1 = 0.05V$ ;  $E_2 = 0.65V$ ;  $E_3 = -0.95V$ ; sensibility = 0.1  $\mu$ C; integration = 0.28-0.48s; flow medium A = 0.15 M NaOH; flow medium B = 1 M NaAc in 0.15 M NaOH; gradient: 10 min 100% A; 2 min linear increase from 0% B to 100% B; 2 min 100% B; 2 min linear increase from = 0% A to 100% A; 5 min A. The samples were desalinated and filtered (microcon 10, amicon, Beverly, USA) before application. The flow speed was 1 ml  $min^{-1}$ . In a few extracts, high-molecular inulin could be found (cf. Figure 1).

#### Example 2: Sequence analysis of the cDNA insert of the plasmid pCy3

A cDNA insert from a pA7 derivative (pCy3) which had mediated the synthesis of high-molecular inulin in the protoplast assay was sequences by means of the dideoxynucleotide technique (Sanger, Proc. Natl. Acad. Sci. USA 74 (1977), 5463-5467). The insert of the clone pCy3 is a DNA with a length of 2073 bp. The nucleotide sequence is indicated under SEQ ID No. 1. The corresponding amino acid sequence is indicated under SEQ ID No. 2. SEQ ID No. 3 is a variant of SEQ ID No. 1 which encodes the same protein as that encoded by SEQ ID No. 1. A sequence analysis and a comparison with already published sequences has shown that the sequence indicated under SEQ ID No. 1 is novel and comprises a coding region exhibiting homologies to FFTs from other organisms.

**Example 3: Synthesis of the plasmid p35-csFFT and integration of the plasmid into the potato genome**

The plasmid p35-csFFT (Figure 2) contains three fragments A, B and C within the binary vector pBin19 (Bevan, Nucl. Acids Res. 12 (1984), 8711, modified according to Becker, Nucleic Acids Res. 18 (1990), 203).

The fragment A contains the 35S promoter of the Cauliflower-Mosaic virus (CaMV). It contains the nucleotides 7146 to 7464 (Gardner, Nucleic Acids Res. 9 (1981), 2871-2888) as an insert between the EcoRI and the SacI site of the polylinker of pBin19-Hyg.

The fragment B contains the nucleotides 1 to 2073 of the sequence SEQ ID No. 1. The fragment B was obtained as a Not I fragment from the vector pBK-CMV into which it was inserted at the EcoRI site via an EcoRI/Not I linker sequence. The fragment C contains the polyadenylation signal of the gene 3 of the T-DNA of the Ti plasmid pTi ACH 5 (Gielen, EMBO J. 3 (1984), 835-846), nucleotide 11749 to 11939, which was isolated as a Pvu II-Hind III fragment from the plasmid pAGV 40 (Herrera-Estrella, Nature 303 (1983), 209-213) and cloned between the SphI and the Hind III site of the polylinker of pBin19-Hyg after adding Sph I linkers to the Pvu II site.

The plasmid p35-csSST was introduced into Agrobacteria (Höfgen and Willmitzer, Nucleic Acids Res. 16 (1988), 9877) and subsequently introduced into potato plants via the Agrobacterium-mediated gene transfer according to the above-described standard techniques. Said potato plants were transformed with a DNA sequence encoding an SST from artichoke (see German patent application DE-A1 197 08 774) and which express these sequences under the control of the 35S promoter. Intact plants were regenerated from transformed cells. Extracts were obtained from the leaves of regenerated plants and examined with respect to the presence of fructosyl polymers. The analysis was carried out as described in Example 1. The analysis of leaves from a range of plants transformed with this vector system unambiguously proved the occurrence of high-molecular inulin, which results from the expression of the FFT gene from artichoke contained in p35-csFFT (cf. Figure 3).

**Table I**

Analysis of inulin content of transgenic potato tubers expressing an artichoke SST and FFT gene

Plant No.	fructan content μmol fructose/ g fresh weight	average degree of polymerization (fructose/glucose ration)
35-SST/FFT 22/26	30.81	21 (20/1)
35-SST/FFT 36/17	27.34	20 (19/1)

**Example 4: Production of the plasmid p33-csFFT and integration of the plasmid into the potato genome**

The plasmid p33-csFFT (Figure 4) is identical with the plasmid p35-csFFT, with the exception that the fragment A contains the B33 promoter of the patatin gene b33 from potato instead of the 35S promoter of CaMV. It contains a DraI fragment (position -1512 to position +14) of the patatin gene b33 (Rocha-Sosa, EMBO J. 8 (1989), 23-29), which was inserted between the EcoRI and the SacI site of the polylinker of pBin19-Hyg. The plasmid p33-csFFT has a size of approximately 14 kb. The plasmid p33-csSST was introduced into potato plants via the Agrobacterium-mediated gene transfer, as described in Example 3. Said potato plants were transformed with a DNA sequence encoding an SST from artichoke (see German patent application E-A1 197 08 774) and which expressed these sequences under the control of the B33 promoter. Intact plants were regenerated from transformed cells. The analysis of tubers from a range of plants transformed with this vector system unambiguously proved the occurrence of high-molecular inulin, which results from the expression of the FFT gene from artichoke contained in p33-csFFT (cf. Figure 5).

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: Max-Planck-Gesellschaft zur Förderung der Wissenschaften, e.V.
- (B) STREET: none
- (C) CITY: Berlin
- (D) STATE: none
- (E) COUNTRY: Germany
- (F) POSTAL CODE: none

(ii) TITLE OF THE INVENTION: Nucleic acid molecules which encode proteins having fructosyl transferase activity and methods for producing long-chain inulin

(iii) NUMBER OF SEQUENCES: 4

## (iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2073 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single stranded
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) POSITION: 21..1872

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TTACCTCATT TCCATCAACC ATG AGA ACG ACT GAA CCC CAA ACT GAC CTT	50
Met Arg Thr Thr Glu Pro Gln Thr Asp Leu	
1                   5                   10	

GAG CAT GCA CCC AAC CAC ACT CCA CTA CTG GAC CAC CCC GAA CCA CCA	98
Glu His Ala Pro Asn His Thr Pro Leu Leu Asp His Pro Glu Pro Pro	
15               20               25	

CCG GCC GCC GTG AGA AAC CGG TTG TTG ATT AGG GTT TCG TCC AGT ATC Pro Ala Ala Val Arg Asn Arg Leu Leu Ile Arg Val Ser Ser Ser Ile 30 35 40	146
ACA TTG GTC TCT CTG TTT TTT GTT TCA GCA TTC CTA CTC ATT CTC CTG Thr Leu Val Ser Leu Phe Phe Val Ser Ala Phe Leu Leu Ile Leu Leu 45 50 55	194
TAC CAA CAC GAT TCC ACT TAC ACC GAT GAT AAT TCA GCA CCG TCG GAA Tyr Gln His Asp Ser Thr Tyr Thr Asp Asp Asn Ser Ala Pro Ser Glu 60 65 70	242
AGT TCT TCC CAG CAG CCC TCC GCT GCC GAT CGC CTG AGA TGG GAG AGA Ser Ser Ser Gln Gln Pro Ser Ala Ala Asp Arg Leu Arg Trp Glu Arg 75 80 85 90	290
ACA GCT TTT CAT TTC CAG CCC GCC AAA AAT TTC ATT TAT GAT CCC AAC Thr Ala Phe His Phe Gln Pro Ala Lys Asn Phe Ile Tyr Asp Pro Asn 95 100 105	338
GGT CCA TTG TTC CAT ATG GGT TGG TAC CAT CTT TTC TAC CAA TAC AAC Gly Pro Leu Phe His Met Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn 110 115 120	386
CCG TAC GCA CCG TTT TGG GGC AAC ATG ACA TGG GGT CAC GCC GTG TCC Pro Tyr Ala Pro Phe Trp Gly Asn Met Thr Trp Gly His Ala Val Ser 125 130 135	434
AAA GAC ATG ATC AAC TGG TTC GAG CTT CCG ATC GCC TTG GCC CCA ACC Lys Asp Met Ile Asn Trp Phe Glu Leu Pro Ile Ala Leu Ala Pro Thr 140 145 150	482
GAA TGG TAC GAT ATC GAG GGT GTT TTA TCA GGC TCA ACC ACG ATC CTC Glu Trp Tyr Asp Ile Glu Gly Val Leu Ser Gly Ser Thr Thr Ile Leu 155 160 165 170	530
CCT GAT GGT CGA ATC TTT GCT CTC TAT ACC GGA AAC ACA AAC GAT CTC Pro Asp Gly Arg Ile Phe Ala Leu Tyr Thr Gly Asn Thr Asn Asp Leu 175 180 185	578
GAG CAA CTT CAA TGC AAA GCC GTG CCA GTT AAT GCA TCC GAC CCA CTT Glu Gln Leu Gln Cys Lys Ala Val Pro Val Asn Ala Ser Asp Pro Leu 190 195 200	626
CTT GTT GAA TGG GTC AGG TAC GAT GCT AAC CCG ATC CTG TAT GCT CCA Leu Val Glu Trp Val Arg Tyr Asp Ala Asn Pro Ile Leu Tyr Ala Pro 205 210 215	674
TCA GGG ATC GGG TTA ACA GAT TAC CGG GAC CCG TCA ACA GTT TGG ACG Ser Gly Ile Gly Leu Thr Asp Tyr Arg Asp Pro Ser Thr Val Trp Thr 220 225 230	722
GGT CCC GAT GGA AAA CAT CGG ATG ATC ATA GGG ACT AAA CGA AAT ACT Gly Pro Asp Gly Lys His Arg Met Ile Ile Gly Thr Lys Arg Asn Thr 235 240 245 250	770

ACA GGA CTC GTA CTT GTA TAC CAT ACC ACC GAT TTC ACA AAC TAC GTA Thr Gly Leu Val Leu Val Tyr His Thr Thr Asp Phe Thr Asn Tyr Val 255	260	265	818	
ATG TTG GAC GAG CCG TTG CAC TCG GTC CCC AAC ACT GAT ATG TGG GAA Met Leu Asp Glu Pro Leu His Ser Val Pro Asn Thr Asp Met Trp Glu 270	275	280	866	
TGT GTC GAC CTT TAC CCT GTG TCA ACG ACC AAC GAT AGT GCA CTT GAT Cys Val Asp Leu Tyr Pro Val Ser Thr Thr Asn Asp Ser Ala Leu Asp 285	290	295	914	
GTT GCG GCC TAT GGT CCG GGT ATC AAG CAT GTG CTT AAA GAA AGT TGG Val Ala Ala Tyr Gly Pro Gly Ile Lys His Val Leu Lys Glu Ser Trp 300	305	310	962	
GAG GGA CAC GCG ATG GAC TTT TAC TCG ATC GGG ACA TAC GAT GCA TTT Glu Gly His Ala Met Asp Phe Tyr Ser Ile Gly Thr Tyr Asp Ala Phe 315	320	325	330	1010
AAC GAT AAG TGG ACA CCC GAT AAT CCC GAA CTA GAC GTC GGT ATC GGG Asn Asp Lys Trp Thr Pro Asp Asn Pro Glu Leu Asp Val Gly Ile Gly 335	340	345	1058	
TTG CGG TGC GAT TAC GGA AGG TTC TTT GCG TCG AAG AGC CTC TAC GAC Leu Arg Cys Asp Tyr Gly Arg Phe Ala Ser Lys Ser Leu Tyr Asp 350	355	360	1106	
CCG TTG AAG AAA CGA AGA GTC ACT TGG GGT TAT GTT GCG GAA TCC GAC Pro Leu Lys Lys Arg Arg Val Thr Trp Gly Tyr Val Ala Glu Ser Asp 365	370	375	1154	
AGT TAC GAC CAA GAC GTC TCT AGA GGA TGG GCT ACT ATT TAT AAT GTT Ser Tyr Asp Gln Asp Val Ser Arg Gly Trp Ala Thr Ile Tyr Asn Val 380	385	390	1202	
GCA AGG ACC ATT GTA CTC GAT CGG AAG ACT GGA ACC CAT CTA CTT CAA Ala Arg Thr Ile Val Leu Asp Arg Lys Thr Gly Thr His Leu Leu Gln 395	400	405	410	1250
TGG CCG GTG GAG GAA ATC GAG AGC TTG AGA TCC AAC GGT CAT GAA TTC Trp Pro Val Glu Glu Ile Glu Ser Leu Arg Ser Asn Gly His Glu Phe 415	420	425	1298	
AAA AAT ATA ACA CTT GAG CCG GGC TCG ATC ATT CCC CTC GAC GTA GGC Lys Asn Ile Thr Leu Glu Pro Gly Ser Ile Ile Pro Leu Asp Val Gly 430	435	440	1346	
TCA GCT ACG CAG TTG GAC ATC GTT GCA ACA TTT GAG GTG GAT CAA GAG Ser Ala Thr Gln Leu Asp Ile Val Ala Thr Phe Glu Val Asp Gln Glu 445	450	455	1394	
GCG TTA AAA GCA ACA AGT GAC ACG AAC GAC GAA TAC GGT TGC ACC ACA Ala Leu Lys Ala Thr Ser Asp Thr Asn Asp Glu Tyr Gly Cys Thr Thr 460	465	470	1442	
			1154	

AGT TCG GGT GCA GCC AAA GGG GAA GTT TTG GAC CAT TCG GGG ATT GCA Ser Ser Gly Ala Ala Lys Gly Glu Val Leu Asp His Ser Gly Ile Ala 475 480 485 490	1490
GTT CTT GCC CAC GGA ACC CTT TCG GAG TTA ACT CCG GTG TAT TTC TAC Val Leu Ala His Gly Thr Leu Ser Glu Leu Thr Pro Val Tyr Phe Tyr 495 500 505	1538
ATT GCT AAA AAC ACC AAG GGA GGT GTG GAT ACA CAT TTT TGT ACG GAT Ile Ala Lys Asn Thr Lys Gly Gly Val Asp Thr His Phe Cys Thr Asp 510 515 520	1586
AAA CTA AGG TCA TCA TAT GAT TAT GAT GGT GAG AAG GTG GTG TAT GGC Lys Leu Arg Ser Ser Tyr Asp Tyr Asp Gly Glu Lys Val Val Tyr Gly 525, 530 535	1634
AGC ACC GTC CCA GTG CTC GAC GGC GAA GAA TTC ACA ATG AGG ATA TTG Ser Thr Val Pro Val Leu Asp Gly Glu Glu Phe Thr Met Arg Ile Leu 540 545 550	1682
GTG GAT CAT TCG GTG GTG GAG GGG TTT GCA CAA GGG GGA AGG ACA GTA Val Asp His Ser Val Val Glu Gly Phe Ala Gln Gly Gly Arg Thr Val 555 560 565 570	1730
ATA ACG TCA AGA GTG TAT CCC ACG AAA GCA ATA TAC GAA GCA GCC AAG Ile Thr Ser Arg Val Tyr Pro Thr Lys Ala Ile Tyr Glu Ala Ala Lys 575 580 585	1778
CTT TTC GTC TTC AAC AAT GCC ACT ACG ACC AGT GTG AAG GCG ACT CTC Leu Phe Val Phe Asn Asn Ala Thr Thr Ser Val Lys Ala Thr Leu 590 595 600	1826
AAG GTC TGG CAA ATG TCT CAA GCC TTT GTC AAG GCT TAT CCG TTT T Lys Val Trp Gln Met Ser Gln Ala Phe Val Lys Ala Tyr Pro Phe 605 610 615	1872
AGTTTTTTAT GCATTTTTT AAGACATTGT TGTTTCATAT GATTCAAGTT TTATCTGTGT	1932
GTTATGTTAA GACACGCAGC TTAAAAATAGC CACATGTGAG ATCATTGCG TATGGCCGTC	1992
AACTATTTTT TAATATGCAA CTTCAGTAAT GCTATTTACA GTATGTTTA AGGAAAAAAA	2052
AAAAAAAAAAA AAAAAAAAAA A	2073

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Arg Thr Thr Glu Pro Gln Thr Asp Leu Glu His Ala Pro Asn His  
1 5 10 15

Thr Pro Leu Leu Asp His Pro Glu Pro Pro Pro Ala Ala Val Arg Asn  
20 25 30

Arg Leu Leu Ile Arg Val Ser Ser Ser Ile Thr Leu Val Ser Leu Phe  
35 40 45

Phe Val Ser Ala Phe Leu Leu Ile Leu Tyr Gln His Asp Ser Thr  
50 55 60

Tyr Thr Asp Asp Asn Ser Ala Pro Ser Glu Ser Ser Ser Gln Gln Pro  
65 70 75 80

Ser Ala Ala Asp Arg Leu Arg Trp Glu Arg Thr Ala Phe His Phe Gln  
85 90 95

Pro Ala Lys Asn Phe Ile Tyr Asp Pro Asn Gly Pro Leu Phe His Met  
100 105 110

Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Tyr Ala Pro Phe Trp  
115 120 125

Gly Asn Met Thr Trp Gly His Ala Val Ser Lys Asp Met Ile Asn Trp  
130 135 140

Phe Glu Leu Pro Ile Ala Leu Ala Pro Thr Glu Trp Tyr Asp Ile Glu  
145 150 155 160

Gly Val Leu Ser Gly Ser Thr Thr Ile Leu Pro Asp Gly Arg Ile Phe  
165 170 175

Ala Leu Tyr Thr Gly Asn Thr Asn Asp Leu Glu Gln Leu Gln Cys Lys  
180 185 190

Ala Val Pro Val Asn Ala Ser Asp Pro Leu Leu Val Glu Trp Val Arg  
195 200 205

Tyr Asp Ala Asn Pro Ile Leu Tyr Ala Pro Ser Gly Ile Gly Leu Thr  
210 215 220

Asp Tyr Arg Asp Pro Ser Thr Val Trp Thr Gly Pro Asp Gly Lys His  
225 230 235 240

Arg Met Ile Ile Gly Thr Lys Arg Asn Thr Thr Gly Leu Val Leu Val  
245 250 255

Tyr His Thr Thr Asp Phe Thr Asn Tyr Val Met Leu Asp Glu Pro Leu  
260 265 270

His Ser Val Pro Asn Thr Asp Met Trp Glu Cys Val Asp Leu Tyr Pro  
275 280 285

Val Ser Thr Thr Asn Asp Ser Ala Leu Asp Val Ala Ala Tyr Gly Pro  
290 295 300

Gly Ile Lys His Val Leu Lys Glu Ser Trp Glu Gly His Ala Met Asp  
305                310                315                320

Phe Tyr Ser Ile Gly Thr Tyr Asp Ala Phe Asn Asp Lys Trp Thr Pro  
325                330                335

Asp Asn Pro Glu Leu Asp Val Gly Ile Gly Leu Arg Cys Asp Tyr Gly  
340                345                350

Arg Phe Phe Ala Ser Lys Ser Leu Tyr Asp Pro Leu Lys Lys Arg Arg  
355                360                365

Val Thr Trp Gly Tyr Val Ala Glu Ser Asp Ser Tyr Asp Gln Asp Val  
370                375                380

Ser Arg Gly Trp Ala Thr Ile Tyr Asn Val Ala Arg Thr Ile Val Leu  
385                390                395                400

Asp Arg Lys Thr Gly Thr His Leu Leu Gln Trp Pro Val Glu Glu Ile  
405                410                415

Glu Ser Leu Arg Ser Asn Gly His Glu Phe Lys Asn Ile Thr Leu Glu  
420                425                430

Pro Gly Ser Ile Ile Pro Leu Asp Val Gly Ser Ala Thr Gln Leu Asp  
435                440                445

Ile Val Ala Thr Phe Glu Val Asp Gln Glu Ala Leu Lys Ala Thr Ser  
450                455                460

Asp Thr Asn Asp Glu Tyr Gly Cys Thr Thr Ser Ser Gly Ala Ala Lys  
465                470                475                480

Gly Glu Val Leu Asp His Ser Gly Ile Ala Val Leu Ala His Gly Thr  
485                490                495

Leu Ser Glu Leu Thr Pro Val Tyr Phe Tyr Ile Ala Lys Asn Thr Lys  
500                505                510

Gly Gly Val Asp Thr His Phe Cys Thr Asp Lys Leu Arg Ser Ser Tyr  
515                520                525

Asp Tyr Asp Gly Glu Lys Val Val Tyr Gly Ser Thr Val Pro Val Leu  
530                535                540

Asp Gly Glu Glu Phe Thr Met Arg Ile Leu Val Asp His Ser Val Val  
545                550                555                560

Glu Gly Phe Ala Gln Gly Arg Thr Val Ile Thr Ser Arg Val Tyr  
565                570                575

Pro Thr Lys Ala Ile Tyr Glu Ala Ala Lys Leu Phe Val Phe Asn Asn  
580                585                590

Ala Thr Thr Thr Ser Val Lys Ala Thr Leu Lys Val Trp Gln Met Ser  
595                600                605

Gln Ala Phe Val Lys Ala Tyr Pro Phe  
610 615

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2073 base pairs
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- ii) MOLECULE TYPE: genomic DNA
- iii) HYPOTHETICAL: YES
- ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) POSITION: 21..1872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCG TAC GCT CCC TTT TGG GGA AAC ATG ACT TGG GGA CAT GCC GTC AGT Pro Tyr Ala Pro Phe Trp Gly Asn Met Thr Trp Gly His Ala Val Ser 740 745 750 755	434
AAG GAT ATG ATA AAT TGG TTT GAA TTA CCG ATA GCC TTA GCG CCA ACT Lys Asp Met Ile Asn Trp Phe Glu Leu Pro Ile Ala Leu Ala Pro Thr 760 765 770	482
GAG TGG TAC GAC ATA GAA GGT GTT CTG AGT GGC AGT ACT ACC ATT TTA Glu Trp Tyr Asp Ile Glu Gly Val Leu Ser Gly Ser Thr Thr Ile Leu 775 780 785	530
CCT GAC GGA AGA ATT TTC GCT CTC TAC ACC GGA AAT ACA AAC GAC CTC Pro Asp Gly Arg Ile Phe Ala Leu Tyr Thr Gly Asn Thr Asn Asp Leu 790 795 800	578
GAG CAG CTC CAG TGT AAG GCC GTG CCA GTT AAT GCT AGT GAT CCA TTA Glu Gln Leu Gln Cys Lys Ala Val Pro Val Asn Ala Ser Asp Pro Leu 805 810 815	626
TTG GTA GAA TGG GTT CGC TAC GAT GCC AAT CCG ATA TTA TAT GCC CCT Leu Val Glu Trp Val Arg Tyr Asp Ala Asn Pro Ile Leu Tyr Ala Pro 820 825 830 835	674
AGT GGC ATC GGC CTC ACA GAT TAC AGA GAT CCT AGT ACT GTG TGG ACG Ser Gly Ile Gly Leu Thr Asp Tyr Arg Asp Pro Ser Thr Val Trp Thr 840 845 850	722
GGC CCT GAC GGT AAA CAC CGT ATG ATA ATC GGG ACG AAG AGG AAT ACG Gly Pro Asp Gly Lys His Arg Met Ile Ile Gly Thr Lys Arg Asn Thr 855 860 865	770
ACT GGA CTC GTC TTA GTA TAT CAC ACT ACC GAC TTT ACA AAT TAT GTA Thr Gly Leu Val Leu Val Tyr His Thr Thr Asp Phe Thr Asn Tyr Val 870 875 880	818
ATG TTG GAC GAG CCG TTG CAC TCG GTC CCC AAC ACT GAT ATG TGG GAA Met Leu Asp Glu Pro Leu His Ser Val Pro Asn Thr Asp Met Trp Glu 885 890 895	866
TGT GTC GAC CTT TAC CCT GTG TCA ACG ACC AAC GAT AGT GCA CTT GAT Cys Val Asp Leu Tyr Pro Val Ser Thr Thr Asn Asp Ser Ala Leu Asp 900 905 910 915	914
GTT GCG GCC TAT GGT CCG GGT ATC AAG CAT GTG CTT AAA GAA AGT TGG Val Ala Ala Tyr Gly Pro Gly Ile Lys His Val Leu Lys Glu Ser Trp 920 925 930	962
GAG GGA CAC GCG ATG GAC TTT TAC TCG ATC GGG ACA TAC GAT GCA TTT Glu Gly His Ala Met Asp Phe Tyr Ser Ile Gly Thr Tyr Asp Ala Phe 935 940 945	1010
AAC GAT AAG TGG ACA CCC GAT AAT CCC GAA CTA GAC GTC GGT ATC GGG Asn Asp Lys Trp Thr Pro Asp Asn Pro Glu Leu Asp Val Gly Ile Gly 950 955 960	1058

TTG CCG TGC GAT TAC GGA AGG TTC TTT GCG TCG AAG AGC CTC TAC GAC		1106
Leu Arg Cys Asp Tyr Gly Arg Phe Phe Ala Ser Lys Ser Leu Tyr Asp		
965	970	975
CCG TTG AAG AAA CGA AGA GTC ACT TGG GGT TAT GTT GCG GAA TCC GAC		1154
Pro Leu Lys Lys Arg Arg Val Thr Trp Gly Tyr Val Ala Glu Ser Asp		
980	985	990
995		
AGT TAC GAC CAA GAC GTC TCT AGA GGA TGG GCT ACT ATT TAT AAT GTT		1202
Ser Tyr Asp Gln Asp Val Ser Arg Gly Trp Ala Thr Ile Tyr Asn Val		
1000	1005	1010
GCA AGG ACC ATT GTA CTC GAT CGG AAG ACT GGA ACC CAT CTA CTT CAA		1250
Ala Arg Thr Ile Val Leu Asp Arg Lys Thr Gly Thr His Leu Leu Gln		
1015	1020	1025
TGG CCG GTG GAG GAA ATC GAG AGC TTG AGA TCC AAC GGT CAT GAA TTC		1298
Trp Pro Val Glu Glu Ile Glu Ser Leu Arg Ser Asn Gly His Glu Phe		
1030	1035	1040
AAA AAT ATA ACA CTT GAG CCG GGC TCG ATC ATT CCC CTC GAC GTA GGC		1346
Lys Asn Ile Thr Leu Glu Pro Gly Ser Ile Ile Pro Leu Asp Val Gly		
1045	1050	1055
TCA GCT ACG CAG TTG GAC ATC GTT GCA ACA TTT GAG GTG GAT CAA GAG		1394
Ser Ala Thr Gln Leu Asp Ile Val Ala Thr Phe Glu Val Asp Gln Glu		
1060	1065	1070
1075		
GCG TTA AAA GCA ACA AGT GAC ACG AAC GAC GAA TAC GGT TGC ACC ACA		1442
Ala Leu Lys Ala Thr Ser Asp Thr Asn Asp Glu Tyr Gly Cys Thr Thr		
1080	1085	1090
AGT TCG GGT GCA GCC AAA GGG GAA GTT TTG GAC CAT TCG GGG ATT GCA		1490
Ser Ser Gly Ala Ala Lys Gly Glu Val Leu Asp His Ser Gly Ile Ala		
1095	1100	1105
GTT CTT GCC CAC GGA ACC CTT TCG GAG TTA ACT CCG GTG TAT TTC TAC		1538
Val Leu Ala His Gly Thr Leu Ser Glu Leu Thr Pro Val Tyr Phe Tyr		
1110	1115	1120
1125		
ATT GCT AAA AAC ACC AAG GGA GGT GTG GAT ACA CAT TTT TGT ACG GAT		1586
Ile Ala Lys Asn Thr Lys Gly Gly Val Asp Thr His Phe Cys Thr Asp		
1125	1130	1135
1140		
AAA CTA AGG TCA TCA TAT GAT TAT GAT GGT GAG AAG GTG GTG TAT GGC		1634
Lys Leu Arg Ser Ser Tyr Asp Tyr Asp Gly Glu Lys Val Val Tyr Gly		
1140	1145	1150
1155		
AGC ACC GTC CCA GTG CTC GAC GGC GAA GAA TTC ACA ATG AGG ATA TTG		1682
Ser Thr Val Pro Val Leu Asp Gly Glu Glu Phe Thr Met Arg Ile Leu		
1160	1165	1170
1175		
GTG GAT CAT TCG GTG GTG GAG GGG TTT GCA CAA GGG GGA AGG ACA GTA		1730
Val Asp His Ser Val Val Glu Gly Phe Ala Gln Gly Gly Arg Thr Val		
1175	1180	1185

ATA ACG TCA AGA GTG TAT CCC ACG AAA GCA ATA TAC GAA GCA GCC AAG	1778
Ile Thr Ser Arg Val Tyr Pro Thr Lys Ala Ile Tyr Glu Ala Ala Lys	
1190	1195
	1200
CTT TTC GTC TTC AAC AAT GCC ACT ACG ACC AGT GTG AAG GCG ACT CTC	1826
Leu Phe Val Phe Asn Asn Ala Thr Thr Ser Val Lys Ala Thr Leu	
1205	1210
	1215
AAG GTC TGG CAA ATG TCT CAA GCC TTT GTC AAG GCT TAT CCG TTT T	1872
Lys Val Trp Gln Met Ser Gln Ala Phe Val Lys Ala Tyr Pro Phe	
1220	1225
	1230
AGTTTTTTAT GCATCTTTT AAGACATTGT TGTTTCATAT GATTCAAGTT TTATCTGTGT	1932
GTTATGTTAA GACACGCAGC TTAAAATAGC CACATGTGAG ATCATTTGCG TATGGCCGTC	1992
AACTATTTTT TAATATGCAA CTTCAGTAAT GCTATTTACA GTATGTTTA AGGAAAAAAA	2052
AAAAAAAAA AAAAAAAAAA A	2073

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Arg Thr Thr Glu Pro Gln Thr Asp Leu Glu His Ala Pro Asn His			
1	5	10	15
Thr Pro Leu Leu Asp His Pro Glu Pro Pro Pro Ala Ala Val Arg Asn			
20	25	30	
Arg Leu Leu Ile Arg Val Ser Ser Ser Ile Thr Leu Val Ser Leu Phe			
35	40	45	
Phe Val Ser Ala Phe Leu Leu Ile Leu Leu Tyr Gln His Asp Ser Thr			
50	55	60	
Tyr Thr Asp Asp Asn Ser Ala Pro Ser Glu Ser Ser Ser Gln Gln Pro			
65	70	75	80
Ser Ala Ala Asp Arg Leu Arg Trp Glu Arg Thr Ala Phe His Phe Gln			
85	90	95	
Pro Ala Lys Asn Phe Ile Tyr Asp Pro Asn Gly Pro Leu Phe His Met			
100	105	110	
Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Tyr Ala Pro Phe Trp			
115	120	125	

Gly Asn Met Thr Trp Gly His Ala Val Ser Lys Asp Met Ile Asn Trp  
 130                    135                    140

Phe Glu Leu Pro Ile Ala Leu Ala Pro Thr Glu Trp Tyr Asp Ile Glu  
 145                    150                    155                    160

Gly Val Leu Ser Gly Ser Thr Thr Ile Leu Pro Asp Gly Arg Ile Phe  
 165                    170                    175

Ala Leu Tyr Thr Gly Asn Thr Asn Asp Leu Glu Gln Leu Gln Cys Lys  
 180                    185                    190

Ala Val Pro Val Asn Ala Ser Asp Pro Leu Leu Val Glu Trp Val Arg  
 195                    200                    205

Tyr Asp Ala, Asn Pro Ile Leu Tyr Ala Pro Ser Gly Ile Gly Leu Thr  
 210                    215                    220

Asp Tyr Arg Asp Pro Ser Thr Val Trp Thr Gly Pro Asp Gly Lys His  
 225                    230                    235                    240

Arg Met Ile Ile Gly Thr Lys Arg Asn Thr Thr Gly Leu Val Leu Val  
 245                    250                    255

Tyr His Thr Thr Asp Phe Thr Asn Tyr Val Met Leu Asp Glu Pro Leu  
 260                    265                    270

His Ser Val Pro Asn Thr Asp Met Trp Glu Cys Val Asp Leu Tyr Pro  
 275                    280                    285

Val Ser Thr Thr Asn Asp Ser Ala Leu Asp Val Ala Ala Tyr Gly Pro  
 290                    295                    300

Gly Ile Lys His Val Leu Lys Glu Ser Trp Glu Gly His Ala Met Asp  
 305                    310                    315                    320

Phe Tyr Ser Ile Gly Thr Tyr Asp Ala Phe Asn Asp Lys Trp Thr Pro  
 325                    330                    335

Asp Asn Pro Glu Leu Asp Val Gly Ile Gly Leu Arg Cys Asp Tyr Gly  
 340                    345                    350

Arg Phe Phe Ala Ser Lys Ser Leu Tyr Asp Pro Leu Lys Lys Arg Arg  
 355                    360                    365

Val Thr Trp Gly Tyr Val Ala Glu Ser Asp Ser Tyr Asp Gln Asp Val  
 370                    375                    380

Ser Arg Gly Trp Ala Thr Ile Tyr Asn Val Ala Arg Thr Ile Val Leu  
 385                    390                    395                    400

Asp Arg Lys Thr Gly Thr His Leu Leu Gln Trp Pro Val Glu Glu Ile  
 405                    410                    415

Glu Ser Leu Arg Ser Asn Gly His Glu Phe Lys Asn Ile Thr Leu Glu  
 420                    425                    430

Pro Gly Ser Ile Ile Pro Leu Asp Val Gly Ser Ala Thr Gln Leu Asp  
435 440 445

Ile Val Ala Thr Phe Glu Val Asp Gln Glu Ala Leu Lys Ala Thr Ser  
450 455 460

Asp Thr Asn Asp Glu Tyr Gly Cys Thr Thr Ser Ser Gly Ala Ala Lys  
465 470 475 480

Gly Glu Val Leu Asp His Ser Gly Ile Ala Val Leu Ala His Gly Thr  
485 490 495

Leu Ser Glu Leu Thr Pro Val Tyr Phe Tyr Ile Ala Lys Asn Thr Lys  
500 505 510

Gly Gly Val, Asp Thr His Phe Cys Thr Asp Lys Leu Arg Ser Ser Tyr  
515 520 525

Asp Tyr Asp Gly Glu Lys Val Val Tyr Gly Ser Thr Val Pro Val Leu  
530 535 540

Asp Gly Glu Glu Phe Thr Met Arg Ile Leu Val Asp His Ser Val Val  
545 550 555 560

Glu Gly Phe Ala Gln Gly Gly Arg Thr Val Ile Thr Ser Arg Val Tyr  
565 570 575

Pro Thr Lys Ala Ile Tyr Glu Ala Ala Lys Leu Phe Val Phe Asn Asn  
580 585 590

Ala Thr Thr Ser Val Lys Ala Thr Leu Lys Val Trp Gln Met Ser  
595 600 605

Gln Ala Phe Val Lys Ala Tyr Pro Phe  
610 615

**Claims**

1. Nucleic acid molecules encoding a protein with the enzymatic activity of a fructosyl transferase (FFT) leading to the synthesis of high-molecular fructan polymers, the molecules of which contain on the average more than 20 fructosyl residues, selected from the group consisting of
  - (a) nucleic acid molecules encoding a protein comprising the amino acid sequence indicated under SEQ ID No. 2 and SEQ ID No. 4;
  - (b) nucleic acid molecules comprising the nucleotide sequence indicated under SEQ ID No. 1 or SEQ ID No. 3 or a corresponding ribonucleotide sequence;
  - (c) nucleic acid molecules hybridizing to a complementary strand of the nucleic acid molecule named under (a) or (b) under stringent conditions;
  - (d) nucleic acid molecules comprising a fragment of a nucleotide sequence of (a), (b) or (c).
2. The nucleic acid molecule of claim 1 which is a DNA molecule.
3. The nucleic acid molecule of claim 2 which is a cDNA molecule.
4. The nucleic acid molecule of claim 1 which is an RNA molecule.
5. The nucleic acid molecule of any one of claims 1 to 4 which is derived from artichoke.
6. A vector containing a nucleic acid molecule of any one of claims 1 to 5, under stringent conditions.
7. The vector of claim 6 wherein the nucleic acid molecule is operatively linked to regulatory elements ensuring the transcription and synthesis of a translatable RNA in prokaryotic and/or eukaryotic cells.

8. The vector of claim 7, wherein the regulatory elements are derived from the patatin B33 promoter or the CaMV 35S promoter.
9. A host cell which is transformed with a nucleic acid molecule of any one of claims 1 to 5 or with a vector of any one of claims 6 to 8 or which is derived from such a cell.
10. The host cell of claim 9, which additionally contains a gene encoding a sucrose-dependent sucrose fructosyl transferase (SST).
11. A method for the production of an FFT, in which the host cell of claim 9 is cultivated under conditions allowing for the synthesis of the FFT and in which the FFT is isolated from the cultivated cells and/or from the culture medium.
12. An FFT, encoded by the nucleic acid molecule of any one of claims 1 to 5 or produced by the method of claim 11.
13. A nucleic acid molecule which specifically hybridizes to a nucleic acid molecule of any one of claims 1 to 5 or to a complementary strand thereof.
14. A method for the production of a transformed host cell of claim 9 or 10, in particular of a transgenic plant cell, transgenic plant tissue and transgenic plants, comprising the introduction of a nucleic acid molecule of any one of claims 1 to 5 or of a vector of any one of claims 6 to 8 into the host cell, the plant cell, the plant tissue or the plant.
15. A transformed host cell, transgenic plant cell, plant tissue or plant which contains a nucleic acid molecule of any one of claims 1 to 5 or a vector of any one of claims 6 to 8 or which is obtainable by the method of claim 14, or which is derived from such a cell, tissue or plant.

16. A transformed host cell, transgenic plant cell, plant tissue or plant of claim 15, additionally containing a gene which encodes a sucrose-dependent sucrose fructosyl transferase.
17. A plant containing plant cells or plant tissue of claim 15 or 16.
18. The plant of any one of claims 15 to 17, which is a useful plant.
19. The plant of claim 18, wherein the useful plant is a sucrose-containing plant.
20. Propagation material of a plant of any one of claims 15 to 19, containing the plant cells of claim 15 or 16.
21. Harvest products of a plant of any one of claims 15 to 19 containing a plant cell of claim 15 or 16.
22. A method for the production of long-chain inulin comprising:
  - (a) cultivating a transformed host cell, transgenic plant cell or plant tissue of claim 15 or 16 or a plant of any one of claims 15 to 19 under conditions which allow for the production of an FFT and the conversion of 1-kestose, optionally supplied from the outside, or of an equivalent substrate into long-chain inulin; and
  - (b) recovering the thus produced inulin from the cultivated cells, tissue or plants or from the medium.
23. A method for the production of long-chain inulin comprising:
  - (a) bringing 1-kestose or an equivalent substrate into contact with an FFT of claim 12 under conditions which allow for the conversion into long-chain inulin; and
  - (b) recovering the thus produced inulin.

24. An in vitro method for producing long-chain inulin wherein the substrate sucrose is converted into long-chain inulin by an enzyme combination consisting of an SST and an FFT.
25. Long-chain inulin obtainable from a host cell, plant cell or plant tissue of claim 15 or 16, from a plant of any one of claims 15 to 19, from the propagation material of claim 20 or from the harvest product of claim 21 or by means of a method of any one of claims 22 to 24.
26. Use of the inulin of claim 25 in order to produce surfactants for increasing the viscosity in aqueous systems, as a detergent, as suspending agent, for speeding up sedimentation and for complexing or for binding water.

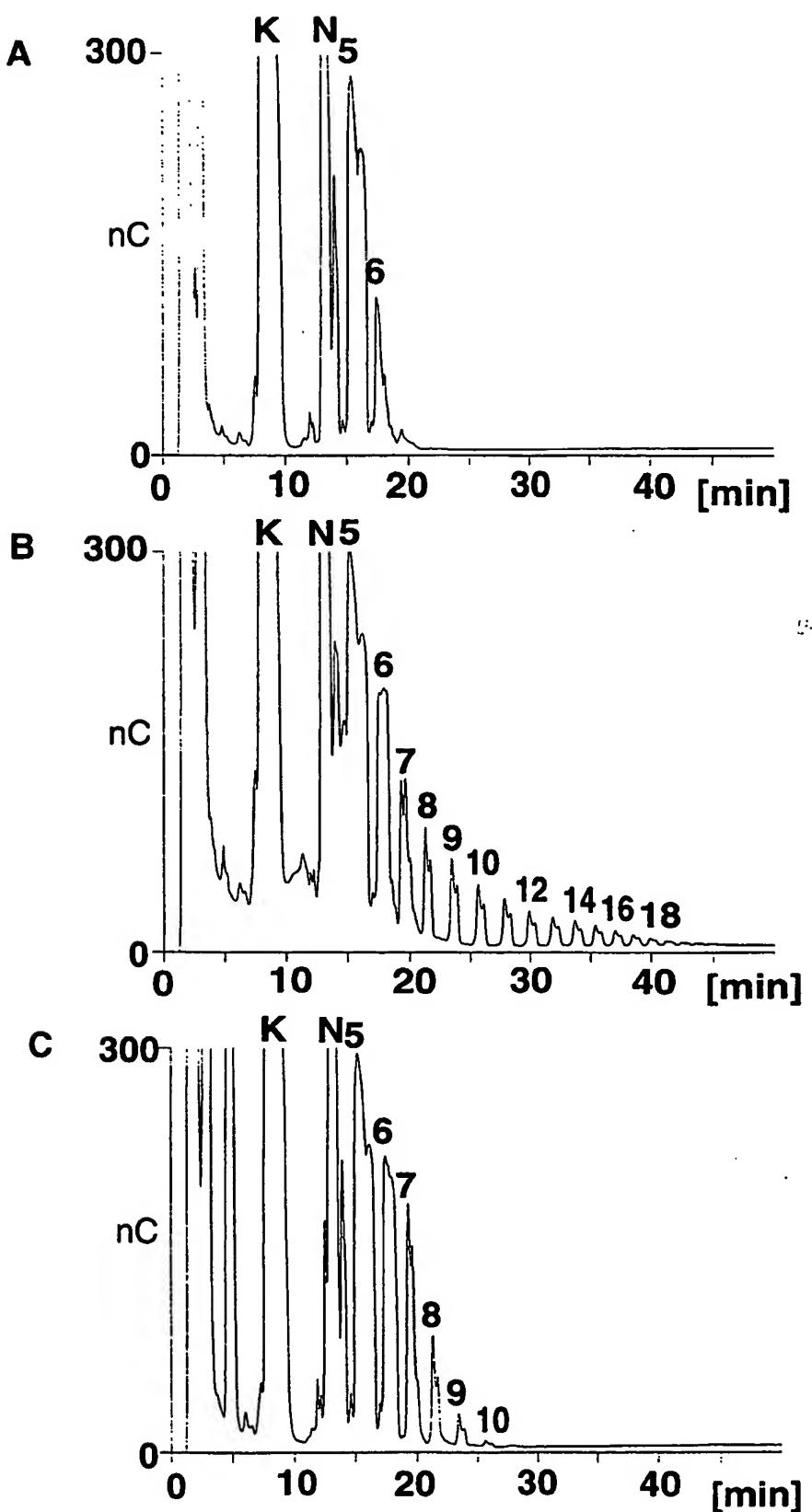


Fig. 1

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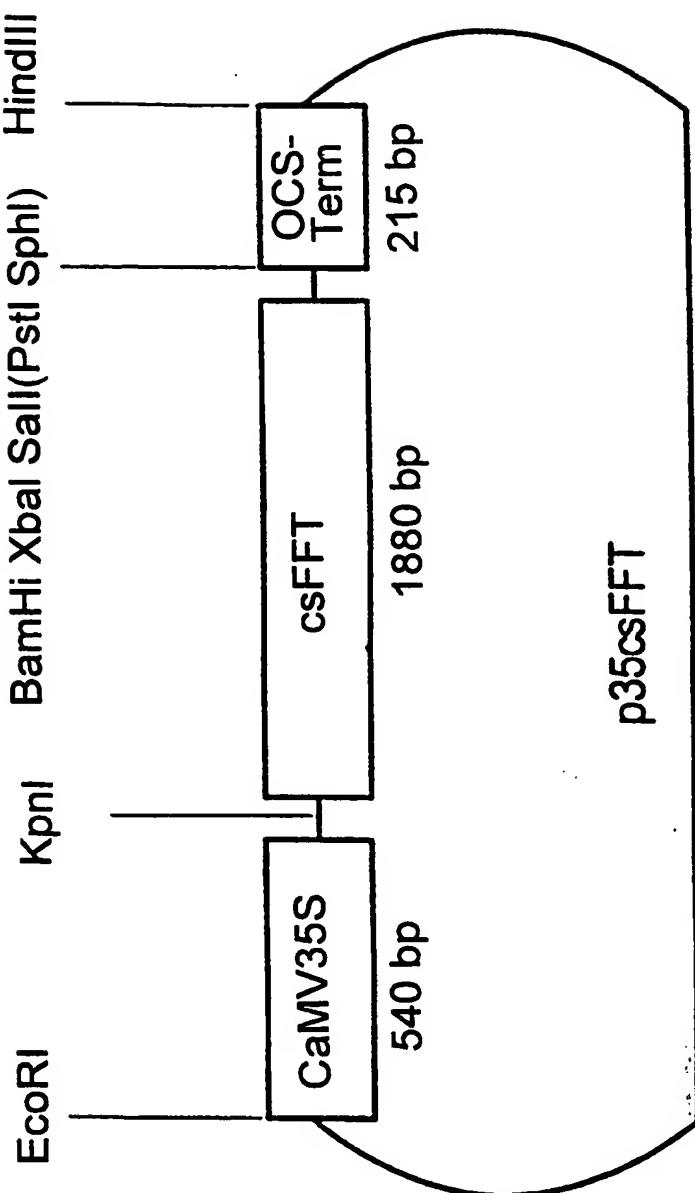
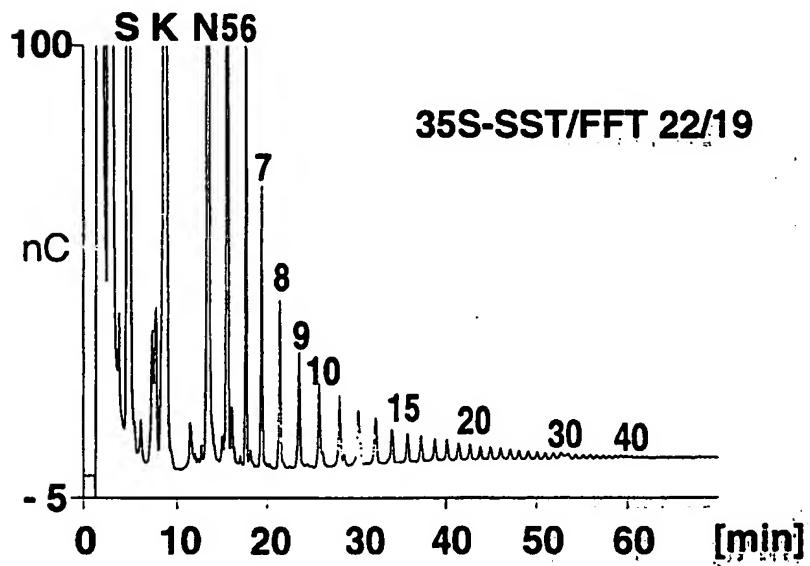
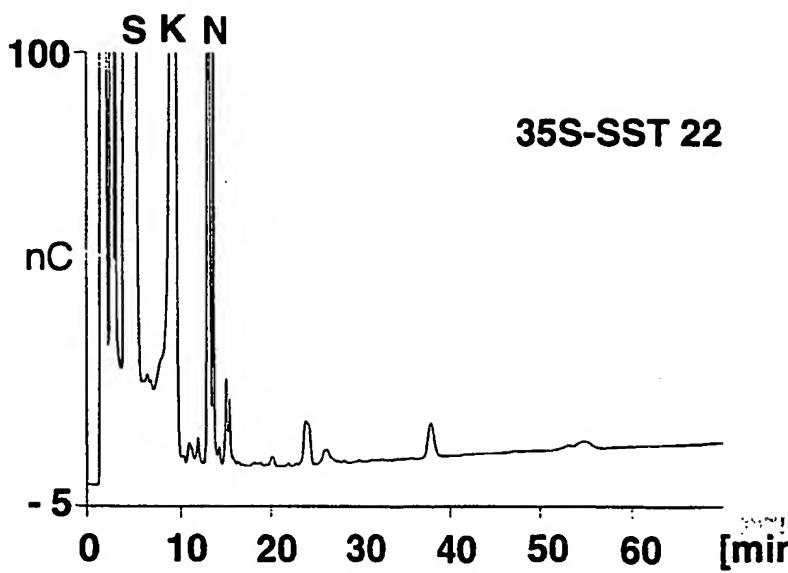


Fig. 2.

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**Fig. 3**

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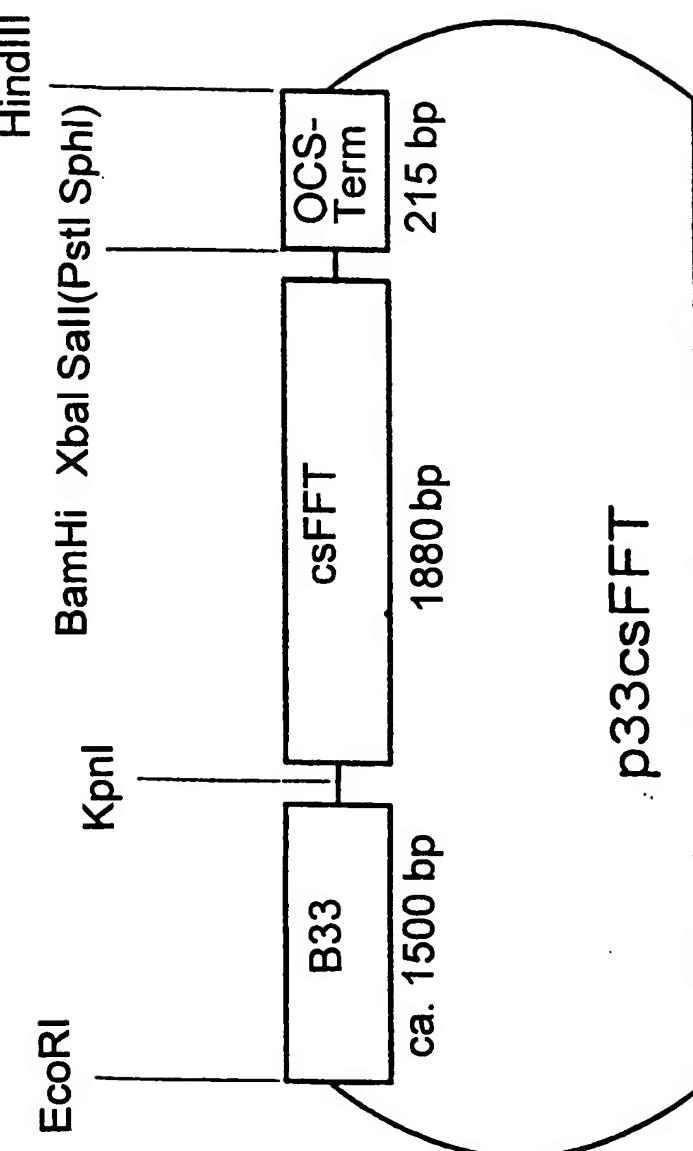
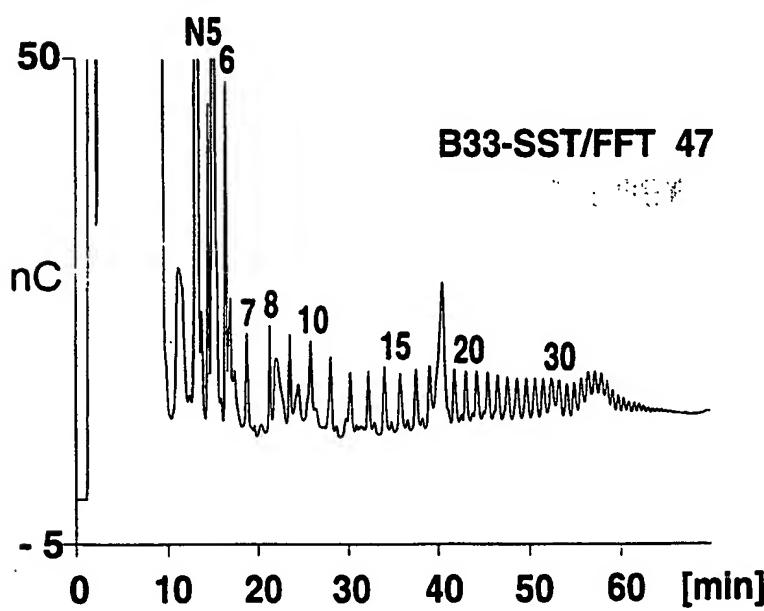
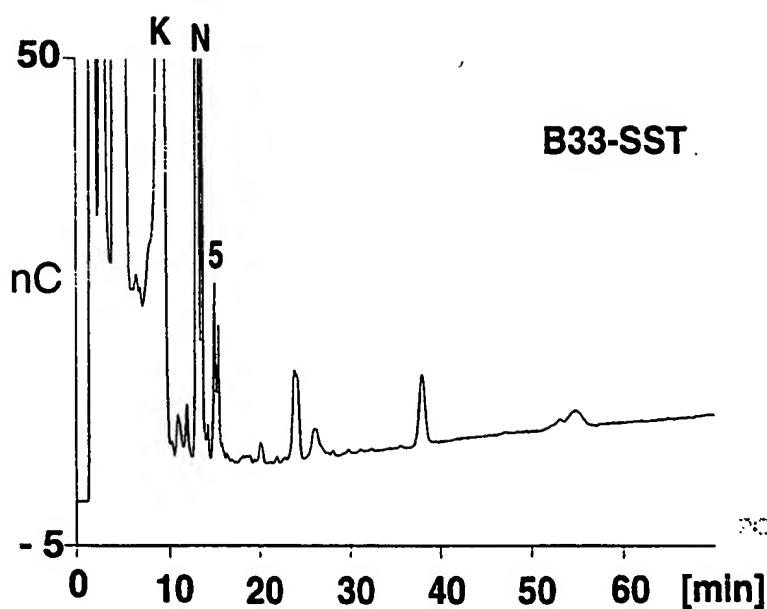


Fig. 4

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**Fig. 5**

# INTERNATIONAL SEARCH REPORT

Inte. onal Application No

PCT/EP 98/07115

A. CLASSIFICATION OF SUBJECT MATTER				
IPC 6	C12N15/82	C12N15/54	C12N9/10	C12N5/10
				A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 96 21023 A (CT VOOR PLANTENVEREDELINGS EN ;TUNEN ARJEN JOHANNES VAN (NL); MEER) 11 July 1996 cited in the application ABSTRACT, PAGE 3, 6,7,11,22,23,24,25	1-9, 11-15, 17-21, 23,25,26 23
Y	---	25
X	WO 94 14970 A (SMEEKENS JOSEPHUS CHRISTIANUS ;WEISBEEK PETRUS JACOBUS (NL); EBSKA) 7 July 1994 PAGES 6,15,17; CLAIMS	25
X	EP 0 627 490 A (SUEDZUCKER AG) 7 December 1994 see the whole document	25,26
	---	-/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

\* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority, claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

12 March 1999

Date of mailing of the international search report

29/03/1999

Name and mailing address of the ISA

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Authorized officer

Holtorf, S

**INTERNATIONAL SEARCH REPORT**

International Application No.

PCT/EP 98/07115

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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